



#6

SEQUENCE LISTING

<110> Xiao, Zhi-Cheng

<120> Peptides, Antibodies Thereto, and Their
Use in the Treatment of Central Nervous System Damage

<130> 0380-P03063US1

<140> US 10/537,648
<141> 2005-06-06<150> PCT/GB2003/005323
<151> 2003-12-05<150> US 60/431,620
<151> 2002-12-06

<160> 35

<170> FastSEQ for Windows Version 4.0

<210> 1
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<212> PRT
<213> Artificial Sequence

<220>

<223> From a phage library that displays random 7-mers

<400> 1
Tyr Leu Thr Gln Pro Gln Ser
1 5<210> 2
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> From a phage library that displays random 7-mers

<400> 2
Gly Ser Leu Pro His Ser Leu
1 5<210> 3
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> From a phage library that displays random 7-mers

<400> 3
Thr Gln Leu Phe Pro Pro Gln
1 5<210> 4
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> From a phage library that displays random 7-mers

<400> 4
His Ser Ile Pro Asp Asn Ile
1 5

<210> 5
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> From a phage library that displays random 7-mers

<400> 5
His His Met Pro His Asp Lys
1 5

<210> 6
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> From a phage library that displays random 7-mers

<400> 6
Tyr Thr Thr Pro Pro Ser Pro
1 5

<210> 7
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> From a phage library that displays random 7-mers

<400> 7
Gln Leu Pro Leu Met Pro Arg
1 5

<210> 8
<211> 508
<212> PRT
<213> Rattus norvegicus

<400> 8
Met Ile Phe Leu Thr Thr Leu Pro Leu Phe Trp Ile Met Ile Ser Ala
1 5 10 15
Ser Arg Gly Gly His Trp Gly Ala Trp Met Pro Ser Ser Ile Ser Ala
20 25 30
Phe Glu Gly Thr Cys Val Ser Ile Pro Cys Arg Phe Asp Phe Pro Asp
35 40 45
Glu Leu Arg Pro Ala Val Val His Gly Val Trp Tyr Phe Asn Ser Pro
50 55 60
Tyr Pro Lys Asn Tyr Pro Pro Val Val Phe Lys Ser Arg Thr Gln Val
65 70 75 80
Val His Glu Ser Phe Gln Gly Arg Ser Arg Leu Leu Gly Asp Leu Gly
85 90 95
Leu Arg Asn Cys Thr Leu Leu Leu Ser Thr Leu Ser Pro Glu Leu Gly
100 105 110
Gly Lys Tyr Tyr Phe Arg Gly Asp Leu Gly Gly Tyr Asn Gln Tyr Thr
115 120 125
Phe Ser Glu His Ser Val Leu Asp Ile Ile Asn Thr Pro Asn Ile Val
130 135 140
Val Pro Pro Glu Val Val Ala Gly Thr Glu Val Glu Val Ser Cys Met
145 150 155 160
Val Pro Asp Asn Cys Pro Glu Leu Arg Pro Glu Leu Ser Trp Leu Gly

165	170	175
His Glu Gly Leu Gly Glu Pro Thr Val	Leu Gly Arg Leu Arg	Glu Asp
180	185	190
Glu Gly Thr Trp Val Gln Val Ser	Leu Leu His Phe Val	Pro Thr Arg
195	200	205
Glu Ala Asn Gly His Arg Leu Gly Cys Gln Ala Ala	Phe Pro Asn Thr	
210	215	220
Thr Leu Gln Phe Glu Gly Tyr Ala Ser	Leu Asp Val Lys Tyr Pro	Pro
225	230	235
Val Ile Val Glu Met Asn Ser Ser Val	Glu Ala Ile Glu Gly	Ser His
245	250	255
Val Ser Leu Leu Cys Gly Ala Asp Ser Asn	Pro Pro Pro	Leu Thr
260	265	270
Trp Met Arg Asp Gly Met Val	Leu Arg Glu Ala Val	Ala Glu Ser Leu
275	280	285
Tyr Leu Asp Leu Glu Glu Val	Thr Pro Ala Glu Asp	Gly Ile Tyr Ala
290	295	300
Cys Leu Ala Glu Asn Ala Tyr Gly Gln Asp	Asn Arg Thr Val	Glu Leu
305	310	315
Ser Val Met Tyr Ala Pro Trp Lys Pro	Thr Val Asn Gly	Thr Val Val
325	330	335
Ala Val Glu Gly Glu Thr Val Ser	Ile Leu Cys Ser Thr	Gln Ser Asn
340	345	350
Pro Asp Pro Ile Leu Thr Ile Phe Lys	Glu Lys Gln Ile	Leu Ala Thr
355	360	365
Val Ile Tyr Glu Ser Gln Leu Gln Leu Glu	Leu Pro Ala Val	Thr Pro
370	375	380
Glu Asp Asp Gly Glu Tyr Trp Cys Val	Ala Glu Asn Gln Tyr	Gly Gln
385	390	395
Arg Ala Thr Ala Phe Asn Leu Ser Val	Glu Phe Ala Pro	Ile Ile Leu
405	410	415
Leu Glu Ser His Cys Ala Ala Ala	Arg Asp Thr Val	Gln Cys Leu Cys
420	425	430
Val Val Lys Ser Asn Pro Glu Pro	Ser Val Ala Phe	Glu Leu Pro Ser
435	440	445
Arg Asn Val Thr Val Asn Glu Thr	Glu Arg Glu Phe	Val Tyr Ser Glu
450	455	460
Arg Ser Gly Leu Leu Leu Thr Ser	Ile Leu Thr	Leu Arg Gly Gln Ala
465	470	475
Gln Ala Pro Pro Arg Val Ile Cys Thr	Ser Arg Asn Leu	Tyr Gly Thr
485	490	495
Gln Ser Leu Glu Leu Pro Phe Gln	Gly Ala His Arg	
500	505	

<210> 9
<211> 205
<212> PRT
<213> Homo sapiens

<400> 9		
Cys Pro Cys Ala Ser Ser Ala Gln Val	Leu Gln Glu Leu Leu	Ser Arg
1	5	10
Ile Glu Met Leu Glu Arg Glu Val	Ser Val Leu Arg Asp	Gln Cys Asn
20	25	30
Ala Asn Cys Cys Gln Glu Ser	Ala Ala Thr Gly Gln	Leu Asp Tyr Ile
35	40	45
Pro His Cys Ser Gly His Gly Asn	Phe Ser Phe Glu	Ser Cys Gly Cys
50	55	60
Ile Cys Asn Glu Gly Trp Phe	Gly Lys Asn Cys Ser	Glu Pro Tyr Cys
65	70	75
Pro Leu Gly Cys Ser Ser Arg	Gly Val Cys Val Asp	Gly Gln Cys Ile
85	90	95
Cys Asp Ser Glu Tyr Ser Gly Asp	Asp Cys Ser Glu	Leu Arg Cys Pro
100	105	110
Thr Asp Cys Ser Ser Arg Gly	Leu Cys Val Asp	Gly Glu Cys Val Cys
115	120	125
Glu Glu Pro Tyr Thr Gly Glu	Asp Cys Arg Glu	Leu Arg Cys Pro Gly
130	135	140
Asp Cys Ser Gly Lys Gly Arg	Cys Ala Asn Gly	Thr Cys Leu Cys Glu
145	150	155
		160

Glu Gly Tyr Val Gly Glu Asp Cys Gly Gln Arg Gln Cys Leu Asn Ala
165 170 175
Cys Ser Gly Arg Gly Gln Cys Glu Glu Gly Leu Cys Val Cys Glu Glu
180 185 190
Gly Tyr Gln Gly Pro Asp Cys Ser Ala Val Ala Pro Pro
195 200 205

<210> 10
<211> 185
<212> PRT
<213> Homo sapiens

<400> 10
Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser Pro
1 5 10 15
Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu
20 25 30
Asp Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp
35 40 45
Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
50 55 60
Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
65 70 75 80
Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
85 90 95
Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro
100 105 110
Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Val
115 120 125
Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro
130 135 140
Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr
145 150 155 160
Pro Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro
165 170 175
Lys Arg Arg Gly Ser Ser Gly Ser Val
180 185

<210> 11
<211> 66
<212> PRT
<213> Homo sapiens

<400> 11
Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly
1 5 10 15
His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu
20 25 30
Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr
35 40 45
Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser
50 55 60
Leu Lys
65

<210> 12
<211> 973
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein

<220>
<221> VARIANT
<222> (509)...(511)
<223> Polyalanine linker

<220>
<221> VARIANT
<222> (717)...(719)
<223> Polyalanine linker

<220>
<221> VARIANT
<222> (905)...(907)
<223> Polyalanine linker

<400> 12
Met Ile Phe Leu Thr Thr Leu Pro Leu Phe Trp Ile Met Ile Ser Ala
1 5 10 15
Ser Arg Gly Gly His Trp Gly Ala Trp Met Pro Ser Ser Ile Ser Ala
20 25 30
Phe Glu Gly Thr Cys Val Ser Ile Pro Cys Arg Phe Asp Phe Pro Asp
35 40 45
Glu Leu Arg Pro Ala Val Val His Gly Val Trp Tyr Phe Asn Ser Pro
50 55 60
Tyr Pro Lys Asn Tyr Pro Pro Val Val Phe Lys Ser Arg Thr Gln Val
65 70 75 80
Val His Glu Ser Phe Gln Gly Arg Ser Arg Leu Leu Gly Asp Leu Gly
85 90 95
Leu Arg Asn Cys Thr Leu Leu Leu Ser Thr Leu Ser Pro Glu Leu Gly
100 105 110
Gly Lys Tyr Tyr Phe Arg Gly Asp Leu Gly Gly Tyr Asn Gln Tyr Thr
115 120 125
Phe Ser Glu His Ser Val Leu Asp Ile Ile Asn Thr Pro Asn Ile Val
130 135 140
Val Pro Pro Glu Val Val Ala Gly Thr Glu Val Glu Val Ser Cys Met
145 150 155 160
Val Pro Asp Asn Cys Pro Glu Leu Arg Pro Glu Leu Ser Trp Leu Gly
165 170 175
His Glu Gly Leu Gly Glu Pro Thr Val Leu Gly Arg Leu Arg Glu Asp
180 185 190
Glu Gly Thr Trp Val Gln Val Ser Leu Leu His Phe Val Pro Thr Arg
195 200 205
Glu Ala Asn Gly His Arg Leu Gly Cys Gln Ala Ala Phe Pro Asn Thr
210 215 220
Thr Leu Gln Phe Glu Gly Tyr Ala Ser Leu Asp Val Lys Tyr Pro Pro
225 230 235 240
Val Ile Val Glu Met Asn Ser Ser Val Glu Ala Ile Glu Gly Ser His
245 250 255
Val Ser Leu Leu Cys Gly Ala Asp Ser Asn Pro Pro Pro Leu Leu Thr
260 265 270
Trp Met Arg Asp Gly Met Val Leu Arg Glu Ala Val Ala Glu Ser Leu
275 280 285
Tyr Leu Asp Leu Glu Glu Val Thr Pro Ala Glu Asp Gly Ile Tyr Ala
290 295 300
Cys Leu Ala Glu Asn Ala Tyr Gly Gln Asp Asn Arg Thr Val Glu Leu
305 310 315 320
Ser Val Met Tyr Ala Pro Trp Lys Pro Thr Val Asn Gly Thr Val Val
325 330 335
Ala Val Glu Gly Glu Thr Val Ser Ile Leu Cys Ser Thr Gln Ser Asn
340 345 350
Pro Asp Pro Ile Leu Thr Ile Phe Lys Glu Lys Gln Ile Leu Ala Thr
355 360 365
Val Ile Tyr Glu Ser Gln Leu Gln Leu Glu Leu Pro Ala Val Thr Pro
370 375 380
Glu Asp Asp Gly Glu Tyr Trp Cys Val Ala Glu Asn Gln Tyr Gly Gln
385 390 395 400
Arg Ala Thr Ala Phe Asn Leu Ser Val Glu Phe Ala Pro Ile Ile Leu
405 410 415
Leu Glu Ser His Cys Ala Ala Ala Arg Asp Thr Val Gln Cys Leu Cys
420 425 430
Val Val Lys Ser Asn Pro Glu Pro Ser Val Ala Phe Glu Leu Pro Ser
435 440 445
Arg Asn Val Thr Val Asn Glu Thr Glu Arg Glu Phe Val Tyr Ser Glu
450 455 460
Arg Ser Gly Leu Leu Leu Thr Ser Ile Leu Thr Leu Arg Gly Gln Ala
465 470 475 480

Gln Ala Pro Pro Arg Val Ile Cys Thr Ser Arg Asn Leu Tyr Gly Thr
 485 490 495
 Gln Ser Leu Glu Leu Pro Phe Gln Gly Ala His Arg Ala Ala Ala Cys
 500 505 510
 Pro Cys Ala Ser Ser Ala Gln Val Leu Gln Glu Leu Leu Ser Arg Ile
 515 520 525
 Glu Met Leu Glu Arg Glu Val Ser Val Leu Arg Asp Gln Cys Asn Ala
 530 535 540
 Asn Cys Cys Gln Glu Ser Ala Ala Thr Gly Gln Leu Asp Tyr Ile Pro
 545 550 555 560
 His Cys Ser Gly His Gly Asn Phe Ser Phe Glu Ser Cys Gly Cys Ile
 565 570 575
 Cys Asn Glu Gly Trp Phe Gly Lys Asn Cys Ser Glu Pro Tyr Cys Pro
 580 585 590
 Leu Gly Cys Ser Ser Arg Gly Val Cys Val Asp Gly Gln Cys Ile Cys
 595 600 605
 Asp Ser Glu Tyr Ser Gly Asp Asp Cys Ser Glu Leu Arg Cys Pro Thr
 610 615 620
 Asp Cys Ser Ser Arg Gly Leu Cys Val Asp Gly Glu Cys Val Cys Glu
 625 630 635 640
 Glu Pro Tyr Thr Gly Glu Asp Cys Arg Glu Leu Arg Cys Pro Gly Asp
 645 650 655
 Cys Ser Gly Lys Gly Arg Cys Ala Asn Gly Thr Cys Leu Cys Glu Glu
 660 665 670
 Gly Tyr Val Gly Glu Asp Cys Gly Gln Arg Gln Cys Leu Asn Ala Cys
 675 680 685
 Ser Gly Arg Gly Gln Cys Glu Glu Gly Leu Cys Val Cys Glu Glu Gly
 690 695 700
 Tyr Gln Gly Pro Asp Cys Ser Ala Val Ala Pro Pro Ala Ala Ala Met
 705 710 715 720
 Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser Pro Pro
 725 730 735
 Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu Asp
 740 745 750
 Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp Leu
 755 760 765
 Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser Ala
 770 775 780
 Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp Phe
 785 790 795 800
 Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala Ala
 805 810 815
 Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro Val
 820 825 830
 Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Val Ser
 835 840 845
 Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro
 850 855 860
 Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr Pro
 865 870 875 880
 Pro Ala Pro Ala Pro Ala Pro Pro Ser Thr Pro Ala Ala Pro Lys
 885 890 895
 Arg Arg Gly Ser Ser Gly Ser Val Ala Ala Ala Arg Ile Tyr Lys Gly
 900 905 910
 Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe Arg Ala
 915 920 925
 Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu Leu Val Gln Lys Tyr
 930 935 940
 Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr Ile Lys Glu Leu Arg
 945 950 955 960
 Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser Leu Lys
 965 970

<210> 13
 <211> 1524
 <212> DNA
 <213> Rattus norvegicus

<400> 13
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cactggggtg cctggatgcc ctgcgtccatc tcagccttcg agggcacgtg tgcgtccatc 120
 ccctggcggtt tcgacttccc ggatgagctc agaccggctg tggtacatgg cgtctggat 180
 ttcaacagtc ctttccccaa gaactaccgg ccagtggctc tcaagtcccg cacacaagtg 240
 gtcacgaga gcttccaggc ccgtagccgc ctgttggag acctgggcct acgaaaactgc 300
 accctgttc tcagcacgtc gagccctgag ctgggaggg aatactattt ccgaggtgac 360
 ctggggcgct acaaccatgtc cacccttcg gacacagcg tcctggatcatcaacacc 420
 cccaacatcg tggtgccccca agaagtgggt gcaggaaacgg aagttagaggt cagctgcatt 480
 gtggccggaca actgcccaga gctgcgcctt gagctgatgg ggctgggcca cgaggggcta 540
 ggggagggca ctgttctggg tcggctgcgg gaggatgaag gcacctgggt gcaggtgtca 600
 ctgctacact tcgtgcctac tagagaggcc aacggccacc gtctggctg tcaggctgcc 660
 ttccccaaaca ccaccttgca gttcgagggt tacgcccattc tggacgtcaa gtacccccc 720
 gtgattgtgg agatgaattt ctctgtggag gccattgagg gctccacgt cagccctgctc 780
 tgggggctg acagcaaccc gccaccgcgtc ctgacttgg tgcggatgg gatgggtgtg 840
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 ggcacatcttgc cttgcctggc agagaatgcc tatggccagg acaaccgcac ggtggagctg 960
 agcgtcatgt atgcaccccttgaagccccaca gtgaatggg cgggtgggtggc ggttagaggg 1020
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 ctgcctttcc agggagacaca ccga 1524

<210> 14
 <211> 615
 <212> DNA
 <213> Homo sapiens

<400> 14
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 gagagggagg tggccatgtg ctgcgtgtt gcaacgcctt actgtgcctt agaaagtgtt 120
 gcaacaggac aactggactt tattcccttac tgcgtggcc acggcaactt tagcttttag 180
 tcctgtggctt gcatctgtt cgaaggctgg tttggcaaga attgtctggg gcccctactgc 240
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 tacagcgggg atgactgttc cgaactccgg tgcccaacag actgcagctc cggggggctc 360
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 gagggctacg ttggtgagga ctgcggccag cggcgtgtt gtaatgcctt cagtggcgaa 540
 ggacaatgtt aggaggggtt ctgcgtctgtt gaagagggtt accagggccc tgactgctca 600
 gcagttggcc ctcca 615

<210> 15
 <211> 555
 <212> DNA
 <213> Homo sapiens

<400> 15
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 cccgcgttca agtaccatgtt cgtgggggg cccggaggacg aggagggaaa agaggaggag 120
 gaagaggagg acgaggacga agacccctggg gagctgggg tggctggagag gaagcccccc 180
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 gccccggctt cccctccccc cccggccaggc gtgagccccc agggagggcc cgtgtggacc 480
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 tcctcggtt cagtgtt 555

<210> 16
 <211> 198
 <212> DNA
 <213> Homo sapiens

<400> 16
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 gctcttggcc atgtgtactt caccataaaatc gaaatcaggc gcctttttt agttgtatgtt 180
 ttatgttattt ctctgttat 198

<210> 17		
<211> 28		
<212> DNA		
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<223> PCR primer MAG1		
<400> 17	28	
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<210> 18		
<211> 28		
<212> DNA		
<213> Artificial Sequence		
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<223> PCR primer MAG2		
<400> 18	28	
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<210> 19		
<211> 29		
<212> DNA		
<213> Artificial Sequence		
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<223> PCR primer TNR1		
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<212> DNA		
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<223> PCR primer TNR2		
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<210> 21		
<211> 32		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> PCR primer NogoN1		
<400> 21	32	
ttgcggccgc aatggaagac ctggaccagt ct		
<210> 22		
<211> 31		
<212> DNA		
<213> Artificial Sequence		
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<223> PCR primer NogoN2		
<400> 22	31	
aaactgcagc cactgagccc gagggagcccc t		
<210> 23		
<211> 28		
<212> DNA		
<213> Artificial Sequence		

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 <223> PCR primer Nogo66-1
 <400> 23
 aaactgcagc aaggatatac aagggtgt 28
 <210> 24
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> PCR primer Nogo66-2
 <400> 24
 gctctagatc acttcagaga atcaacta 28
 <210> 25
 <211> 2934
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Construct resulting from sequentially connected
 PCR products
 <400> 25
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 tccatccccct gccgtttcga ctccccggat gagctcagac cggtgtggatcatggcgtc 180
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 gtcgccttcc ccaacaccac ctgcgttgc gagggttacg ccagtctggatgtcaagtac 720
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 caggtgtcgc aggagctgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgc 1620
 cgagaccagt gcaaccccaa ctgtgtccaa gaaagtgcgttgcgttgcgttgcgttgcgttgc 1680
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 ggggtgtgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgc 1860
 gaactccggat gccccacaga ctgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgc 1920
 tgtgaagagc cctacactgg cgaggactgc agggaaactgatgcgttgcgttgcgttgcgttgc 1980
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